

1 ATGAGTGGCCTGGGCCGGAGCAGGCGAGGTGGCCGGAGCCGTGTGGACCAAGGAGGAGCGC 60
 1 M S G L G R S R R G G R S R V D Q E E R 20
 .
 61 TTTCCACAGGGCCTGTGGACGGGGTGGCTATGAGATCCTGCCCGAAGAGCAGTACTGG 120
 21 F P Q G L W T G V A M R S C P E E Q Y W 40
 .
 121 GATCCTCTGCTGGTACCTGCATGTCTGCAAAACCATTGCAACCATCAGAGCCAGCGC 180
 41 D P L L G T C M S C K T I C N H Q S Q R 60
 .
 181 ACCTGTGCAGCCTCTGCAGGTCACTCAGCTGCCGAAGGAGCAAGGCAAGTTCTATGAC 240
 61 T C A A F C R S L S C R K E Q G K F Y D 80
 .
 241 CATCTCCTGAGGGACTGCATCAGCTGTGCCTCCATCTGTGGACAGCACCTAACATGT 300
 81 H L L R D C I S C A S I C G Q H P K Q C 100
 .
 301 GCATACTTCTGTGAGAACAGCTCAGGAGCCAGTGAACCTTCCACCAGAGCTCAGGAGA 360
 101 A Y F C E N K L R S P V N L P P E L R R 120
 .
 361 CAGCGGAGTGGAGAAGTTGAAAACAATTAGACAACACTCGGAAGGTACCAAGGATTGGAG 420
 121 Q R S G E V E N N S D N S G R Y Q G L E 140
 .
 421 CACAGAGGCTCAGAACAGCTCAGCTCTCCGGGCTGAAGCTGAGTCAGATCAGGTG 480
 141 H R G S E A S P A L P G L K L S A D Q V 160
 .
 481 GCCCTGGTCTACAGCACGCTGGGGCTCTGCCTGTGTGCCGTCTGCTGCTTCCTGGTG 540
 161 A L V Y S T L G L C L C A V L C C F L V 180
 .
 541 GCGGTGGCCTGCTTCTCAAGAACAGGGGGATCCCTGCTCTGCCAGCCCCGCTCAAGG 600
 181 A V A C F L K K R G D P C S C Q P R S R 200
 .
 601 CCCCGTCAAAGTCCGCCAAGTCTTCCCAGGATCACGCGATGGAAGCCGGCAGCCCTGTG 660
 201 P R Q S P A K S S Q D H A M E A G S P V 220
 .
 661 AGCACATCCCCGAGCCAGTGGAGACCTGCAGCTCTGCTTCCCTGAGTGCAGGGGCC 720
 221 S T S P E P V E T C S F C F P E C R A P 240
 .
 721 ACGCAGGAGAGCGCAGTCACGCCTGGACCCCGACCCCACTTGTGCTGGAAGGTGGGG 780
 241 T Q E S A V T P G T P D P T C A G R W G 260
 .
 781 TGCCACACCAGGACCACAGTCCTGCAGCCTGCCACACATCCCAGACAGTGGCCTGGC 840
 261 C H T R T T V L Q P C P H I P D S G L G 280
 .
 841 ATTGTGTGTGCCTGCCAGGAGGGGGCCAGGTGCATAA 882
 281 I V C V P A Q E G G P G A * 294

FIG. 1

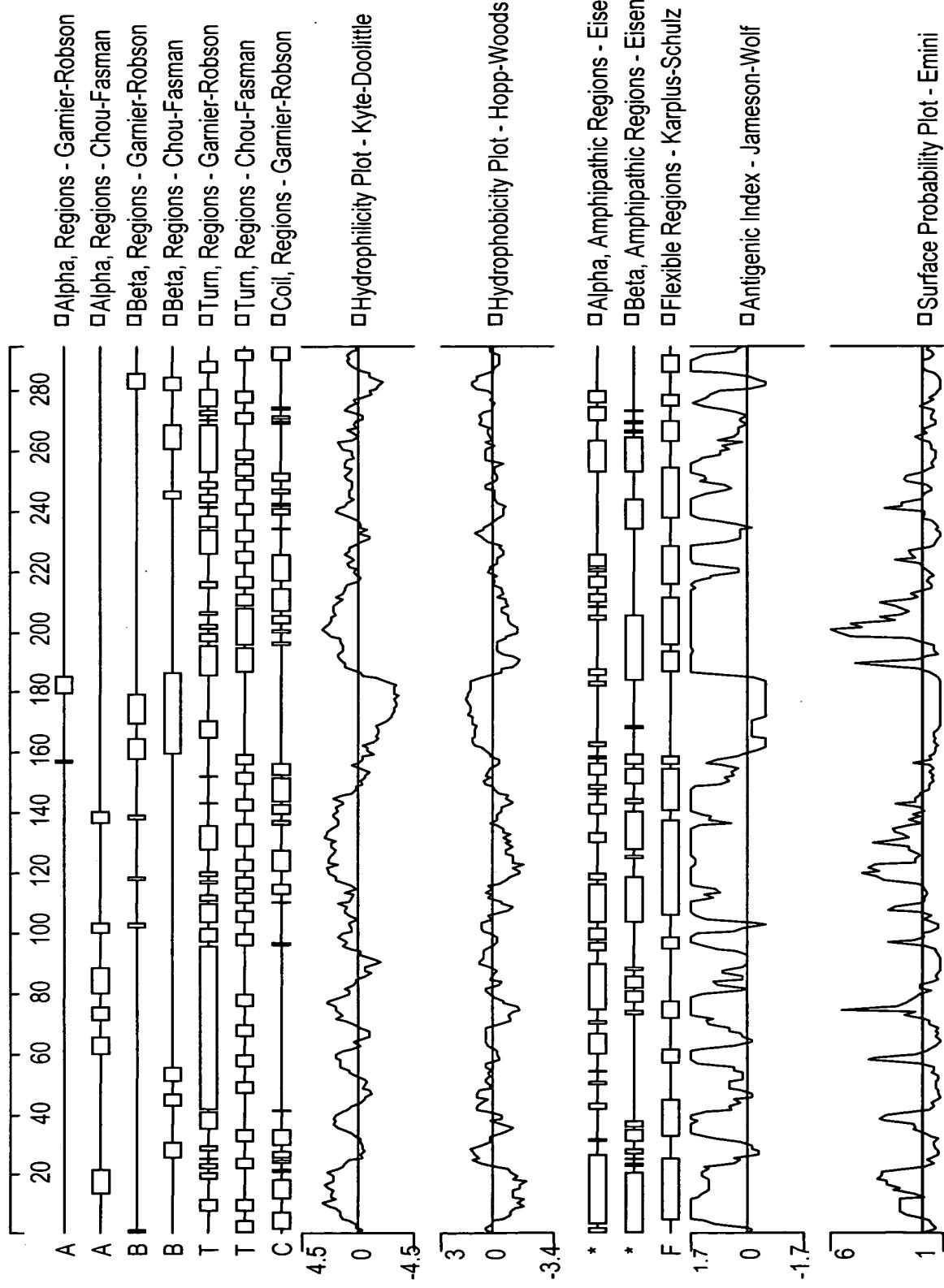


FIG. 2